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SEQUENCE LISTING

<110> Burkly, Linda C.

<120> TREATMENT FOR INSULIN DEPENDENT DIABETES

<130> 10274-008003

<140> US 09/234,290

<141> 1999-01-20

<150> US 08/447,118

<151> 1995-05-22

<150> US 08/029,330

<151> 1993-02-09

<150> PCT/US94/01456

<151> 1994-02-09

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 360

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> pBAG159 insert: HP1/2 heavy chain variable region;
amino acid 1 is Glu (E) but Gln (Q) may be
substituted

<221> CDS

<222> (1)...(360)

<400> 1

gtc aaa ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc tca 48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc tat 96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30

atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att gga 144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
35 40 45

agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc cag 192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln

50	55	60	
gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg ctg			240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu			
65	70	75	80
cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt gca			288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala			
	85	90	95
gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc caa			336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln			
	100	105	110
ggg acc acg gtc acc gtc tcc tca			360
Gly Thr Thr Val Thr Val Ser Ser			
	115	120	

<210> 2
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 2

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser			
1	5	10	15
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr			
	20	25	30
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly			
	35	40	45
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln			
	50	55	60
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu			
	65	70	75
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala			
	85	90	95
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln			
	100	105	110
Gly Thr Thr Val Thr Val Ser Ser			
	115	120	

<210> 3
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> pBAG172 insert: HP1/2 light chain variable region

<221> CDS
 <222> (1)...(318)
 <223> HP1/2 light chain variable region

<400> 3

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agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga      48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
  1              5              10              15

gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat      96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
          20              25              30

gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata      144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
          35              40              45

tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc      192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
          50              55              60

agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct      240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
          65              70              75              80

gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac      288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
          85              90              95

acg ttc gga ggg ggg acc aag ctg gag atc      318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
          100              105

```

<210> 4
 <211> 106
 <212> PRT
 <213> Homo sapiens

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<400> 4
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
  1              5              10              15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
          20              25              30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
          35              40              45
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
          50              55              60
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
          65              70              75              80
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
          85              90              95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
          100              105

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<210> 5
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (1)...(429)

<221> sig_peptide

<222> (1)...(57)

<221> mat_peptide

<222> (58)...(429)

<221> misc_feature

<222> (0)...(0)

<223> pBAG195 insert: AS heavy chain variable region

<400> 5

atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gca cca ggt 48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
-15 -10 -5

gcc cac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga 96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
1 5 10

cct agc cag acc ctg agc ctg acc tgc acc gcg tct ggc ttc aac att 144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
15 20 25

aaa gac acc tat atg cac tgg gtg aga cag cca cct gga cga ggt ctt 192
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30 35 40 45

gag tgg att gga agg att gat cct gcg agt ggc gat act aaa tat gac 240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

ccg aag ttc cag gtc aga gtg aca atg ctg gta gac acc agc agc aac 288
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
65 70 75

cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtc 336
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
80 85 90

tat tat tgt gca gac gga atg tgg gta tca acg gga tat gct ctg gac 384
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
95 100 105

ttc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gag tcc 429
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110 115 120

<210> 6

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1)...(19)

<400> 6

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Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
               -15               -10               -5
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
              1               5               10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
            15              20              25
Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
30              35              40              45
Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
              50              55              60
Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
            65              70              75
Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
            80              85              90
Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
            95              100             105
Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110              115              120

```

<210> 7

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(384)

<221> sig_peptide

<222> (1)...(57)

<221> mat_peptide

<222> (58)...(384)

<221> misc_feature

<222> (0)...(0)

<223> pBAG198 insert: VK2 (SVMDY) light chain variable region

<400> 7

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atg ggt tgg tcc tgc atc atc ctg ttc ctg gtt gct acc gct acc ggt      48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
               -15               -10               -5

gtc cac tcc agc atc gtg atg acc cag agc cca agc agc ctg agc gcc      96
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
              1               5               10

agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag agt gtg      144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
            15              20              25

act aat gat gta gct tgg tac cag cag aag cca ggt aag gct cca aag      192
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys

```

30	35	40	45	
ctg ctg atc tac tat gca tcc aat cgc tac act ggt gtg cca gat aga				240
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg				
	50	55	60	
ttc agc ggt agc ggt tat ggt acc gac ttc acc ttc acc atc agc agc				288
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser				
	65	70	75	
ctc cag cca gag gac atc gcc acc tac tac tgc cag cag gat tat agc				336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser				
	80	85	90	
tct ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt aag				384
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys				
	95	100	105	
tg				386

<210> 8
 <211> 128
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1) ... (19)

E1 cut

<400> 8	
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
	-15 -10 -5
Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
	1 5 10
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val	
	15 20 25
Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
	30 35 40 45
Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	
	50 55 60
Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
	65 70 75
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser	
	80 85 90
Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys	
	95 100 105

<210> 9
 <211> 1347
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1338)
 <221> misc_feature

<222> (1)...(219)
 <223> VCAM-1 gene segment: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc_feature

<222> (220)...(229)

<223> Hinge region: This portion of the sequence corresponds, in part, to Exons I, II and III nucleotide sequence of Cybulsky et al. Proc. Nat'l. Acad. Sci. USA 88: 7861 (1991).

<221> misc_feature

<222> (230)...(338)

<223> Heavy chain constant region 2: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 2 of Human IgG1 heavy chain constant region.

<221> misc_feature

<222> (339)...(446)

<223> Heavy chain constant region 3: This portion of the sequence corresponds, in part, to Fig. 12A in PCT/US92/02050 and represents the heavy chain constant region 3 of Human IgG1 heavy chain constant region.

<400> 9

atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg 48
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
 1 5 10 15

ata atg ttt gca gct tct caa gct ttt aaa atc gag acc acc cca gaa 96
 Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
 20 25 30

tct aga tat ctt gct cag att ggt gac tcc gtc tca ttg act tgc agc 144
 Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
 35 40 45

acc aca ggc tgt gag tcc cca ttt ttc tct tgg aga acc cag ata gat 192
 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
 50 55 60

agt cca ctg aat ggg aag gtg acg aat gag ggg acc aca tct acg ctg 240
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
 65 70 75 80

aca atg aat cct gtt agt ttt ggg aac gaa cac tct tac ctg tgc aca 288
 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
 85 90 95

gca act tgt gaa tct agg aaa ttg gaa aaa gga atc cag gtg gag atc 336
 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile

100	105	110	
tac tct ttt cct aag gat cca gag att cat ttg agt ggc cct ctg gag			384
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu			
115	120	125	
gct ggg aag ccg atc aca gtc aag tgt tca gtt gct gat gta tac cca			432
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro			
130	135	140	
ttt gac agg ctg gag ata gac tta ctg aaa gga gat cat ctc atg aag			480
Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys			
145	150	155	160
agt cag gaa ttt ctg gag gat gca gac agg aag tcc ctg gaa acc aag			528
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys			
165	170	175	
agt ttg gaa gta acc ttt act cct gtc att gag gat att gga aaa gtt			576
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val			
180	185	190	
ctt gtt tgc cga gct aaa tta cac att gat gaa atg gat tct gtg ccc			624
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro			
195	200	205	
aca gta agg cag gct gta aaa gaa ttg caa gtc gac aaa act cac aca			672
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr			
210	215	220	
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc			720
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe			
225	230	235	240
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct			768
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro			
245	250	255	
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc			816
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val			
260	265	270	
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca			864
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr			
275	280	285	
aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc			912
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val			
290	295	300	
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc			960
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys			
305	310	315	320
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc			1008
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser			
325	330	335	

E1
conf

aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca 1056
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350

tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc 1104
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365

aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg 1152
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380


cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac 1200
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg 1248
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac 1296
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1338
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

tgagtgcgg 1347

 <210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 10
 tcgtcgacaa aactcacaca tgcc 24

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 11
 gtaaatgagt gcggcgggccg ccaa 24

<210> 12
 <211> 115

<212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 12
 gcggcgcgcg tccaaccacc aatctcaaag cttggtaccc ggggaattcag atctgcagca 60
 tgctcgagct ctagatatcg attccatgga tcttcacatc ccaatccgcg gccgc 115

<210> 13
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 13
 gagctcgagg cggccgcacc atgcctggga agatggtcgt g 41

<210> 14
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

E1
 <400> 14
 aagtcgactt gcaattcttt tac 23

<210> 15
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 15
 tcgacgcggc cgcg 14

<210> 16
 <211> 446
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
 1 5 10 15
 Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
 20 25 30

Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
 35 40 45
 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
 50 55 60
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
 65 70 75 80
 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
 85 90 95
 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
 100 105 110
 Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
 115 120 125
 Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
 130 135 140
 Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
 145 150 155 160
 Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
 165 170 175
 Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
 180 185 190
 Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
 195 200 205
 Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 17

Asp Lys Thr His Thr Cys

1

5

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 18

Met Pro Gly Lys Met Val Val

1

5